SEQUENCE LISTING

(1)   GENERAL INFORMATION

    (i)   APPLICANT: JACOBSON, Myron K.; JACOBSON, Elaine L.; AMÉ, Jean-Christophe; LIN, Winston

    (ii)   TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZYMES, THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE THEREWITH

    (iii) NUMBER OF SEQUENCES: 38

    (iv)   CORRESPONDENCE ADDRESS:
        (A)   ADDRESSEE: Fulbright & Jaworski L.L.P.
        (B)   STREET: 666 Fifth Avenue
        (C)   CITY: New York
        (D)   STATE: New York
        (E)   COUNTRY: USA
        (F)   ZIP: 10103

    (v)   COMPUTER READABLE FORM:
        (A)   MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
        (B)   COMPUTER: IBM PS/2
        (C)   OPERATING SYSTEM: PC-DOS
        (D)   SOFTWARE: Wordperfect

    (vi)   CURRENT APPLICATION DATA:
        (A)   APPLICATION NUMBER: To Be Assigned
        (B)   FILING DATE: Concurrently Herewith

    (viii) ATTORNEY/AGENT INFORMATION:
        (A)   NAME: John E. Lynch
        (B)   REGISTRATION NUMBER: 20,940
        (C)   REFERENCE/DOCKET NUMBER: NIAD 201-JEL/ES

    (ix)   TELECOMMUNICATION INFORMATION:
        (A)   TELEPHONE: 212-318-3000
        (B)   TELEFAX: 212-752-5958

(2) INFORMATION FOR SEQ ID NO: 1:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4069 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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 121 ctgcagaagc agtcagcggc agaggggggca tggtgccggg aggcaccgag gaggggggcgc
 181 agtccgtccc tcccaggggtt agtgaatgag gctctacgcc cgggctggcc cggagactca
 241 gtgctgcggg tcccagcatg agtgcgggcc ccggctgtga gccctgcacc aagcgacccc
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 361 ggcagaggcg cgtcctcgat tccaaggacg ctccggtgca gttcagggtc ccgccgtcct
 421 cgtcaggctg cgccctgggc cgggcgggac agcaccgagg cagcgccacc tctcttgttt
 481 tcaaacagaa gactataacc agttggatgg acactaaagg aatcaagaca gttgaatcag
 541 aaagtttgca tagtaaagaa aacaacaata caagagaaga atccatgatg agttctgtac
 601 aaaaagataa ctttttatcaa cataacatgg aaaaattaga aaatgtttct cagctaggtt
 661 ttgataagtc accagttgaa aaaggtacac agtatttgaa gcagcatcag actgcggcta
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 781 cggtaactct ggtaccagag cagttcagta atgctaatgt cgatcagtcg tccccaaagg
 841 atgatcacag tgacacaaat agtgaggaga gtagagataa tcagcagttt ttgacacatg
 901 taaagcttgc gaatgcaaag cagacgatgg aagatgaaca gggcagagaa gccagaagcc
 961 accagaagtg tggcaaggct tgccatcctg cagaagcctg tgcaggggtgt cagcaggagg
1021 agacagacgt ggtgtccgag agcccccttgt cggacactgg ctctgaggat gttggtactg
1081 gactgaaaaa tgccaacaga ttgaatagac aagaaagtag tctaggaaat tctcctccat
1141 ttgagaaaga aagtgaacct gagtcaccaa tggatgtaga taattccaaa aatagttgtc
1201 aggattcaga agcagatgaa gagacaagtc caggttttga tgaacaggaa gatagcagtt
1261 ctgctcaaac agcaaataaa ccttcaaggt tccaaccaag agaagctgac actgagttga
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1621 ttggaactcc tattgaggag atgaggagaa tgccaaggtg tgggatccgg ctgcctccct
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1981 ttgatttctg ggataaggta ctagaagaag cagaagctca acacttgtat cagtccatct
2041 tgcctgatat ggtgaaaatt gcactctgtc tgccaaatat ttgtacccag ccaataccac
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2221 ccagttatcc agatattaac ttcaatcggt tgtttgaagg acgttcatca aggaaaccag
2281 agaagcttaa aacgctcttc tgctacttta gaagagtcac agagaaaaaa cccactgggt
2341 tggtgacatt cacaagacag agtcttgaag attttccaga gtgggaaaga tgtgaaaaac
2401 tcctgactcg actgcatgtc acttacgaag gtaccataga aggaaacggc cagggcatgc
2461 tacaggtgga ttttgcaaac cgtttcgttg gaggtggtgt aaccagtgca ggacttgtgc
2521 aagaagaaat ccgcttttta atcaaccctg agttgattgt ttcacggctc ttcactgagg
2581 tgctggatca caatgaatgt cttatcatca caggtactga gcagtacagt gaatacacag
2641 gctatgccga aacataccgc tgggcccgga gccatgaaga caggagcgaa agggacgact
2701 ggcagaggcg cacgactgag atcgtcgcca tcgacgccct ccacttcaga cgctacctcg
2761 accagtttgt gcccgagaag atcagacggg agcttaacaa ggcttactgt ggatttcttc
2821 gtcctggagt ttcttcagag aacctgtctg cagtggctac aggaaactgg ggctgtggtg
2881 cctttggggg tgatgctaga ctaaaagcct aatacagat cctggcagct gctgtagctg
2941 agcgagacgt ggtttatttc acctttgggg actcagaact gatgagagac atttacagca
3001 tgcatacatt cctcactgag aggaaactga ctgttggaga agtatataag ctgctgctac
3061 gatattacaa tgaagaatgc agaaactgct ccaccccccgg accagacatc aagctttatc
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3241 gtgtgaactg acatgatatc catgtgtata taatccgcgt ttgtaggcaa ggatgcagtc
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3481 tttttttgatg cctaaatata caaatcacct ctgcagctag cagatgccac ggaaggtggt
3541 ggaaccctag gagctgtaac tgagtctgct gcagatctcc ctctgagcct ctcaccccta
3601 ccctattatc attgtggtgg tggaggtttt ttgattttg aaataagagt tgggtttgtt
3661 aaataataca gatctcctag gttaagagtt ttatatttaa gaatactttt caaaaagtta
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3781 ttgtattgac tgttttttgga aattgaccca aatgaaagga aatatgagaa taagagtttc
3841 ccaaatggtg tttaaaaaca aacaggttca agacacgcga aggacctcgt ttcctgggat
3901 ttttttttctt tttcttttttt tgaattagga ttattgtttg ttccttggtg cttgagacat
3961 attcatataa ccaaagttta ggaactggga acttcgtggt gatttgtaca tattgaagtt
4021 tctctggtac tcaaaggtta tgtagttaat aaattttcat taacaaaaaa
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(2) INFORMATION FOR SEQ ID NO: 2:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 977 amino acids
             (B) TYPE: protein
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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  1 MSAGPGCEPC TKRPRWDAAA TSPPAASDAR SFPGRQRRVL DSKDAPVQFR VPPSSSGCAL
 61 GRAGQHRGSA TSLVFKQKTI TSWMDTKGIK TVESESLHSK ENNNTREESM MSSVQKDNFY
121 QHNMEKLENV SQLGFDKSPV EKGTQYLKQH QTAAMCKWQN EGPHSERLLE SEPPAVTLVP
181 EQFSNANVDQ SSPKDDHSDT NSEESRDNQQ FLTHVKLANA KQTMEDEQGR EARSHQKCGK
241 ACHPAEACAG CQQEETDVVS ESPLSDTGSE DVGTGLKNAN RLNRQESSLG NSPPFEKESE
301 PESPMDVDNS KNSCQDSEAD EETSPGFDEQ EDSSSAQTAN KPSRFQPREA DTELRKRSSA
361 KGGEIRLHFQ FEGGESRAGM NDVNAKRPGS TSSLNVECRN SKQHGRKDSK ITDHFMRVPK
421 AEDKRKEQCE MKHQRTERKI PKYIPPHLSP DKKWLGTPIE EMRRMPRCGI RLPPLRPSAN
481 HTVTIRVDLL RIGEVPKPFP THFKDLWDNK HVKMPCSEQN LYPVEDENGE RAAGSRWELI
541 QTALLNRLTR PQNLKDAILK YNVAYSKKWD FTALIDFWDK VLEEAEAQHL YQSILPDMVK
601 IALCLPNICT QPIPLLKQKM NHSITMSQEQ IASLLANAFF CTFPRRNAKM KSEYSSYPDI
661 NFNRLFEGRS SRKPEKLKTL FCYFRRVTEK KPTGLVTFTR QSLEDFPEWE RCEKLLTRLH
721 VTYEGTIEGN GQGMLQVDFA NRFVGGGVTS AGLVQEEIRF LINPELIVSR LFTEVLDHNE
781 CLIITGTEQY SEYTGYAETY RWARSHEDRS ERDDWQRRTT EIVAIDALHF RRYLDQFVPE
841 KIRRELNKAY CGFLRPGVSS ENLSAVATGN WGCGAFGGDA RLKALIQILA AAVAERDVVY
901 FTFGDSELMR DIYSMHTFLT ERKLTVGEVY KLLLRYYNEE CRNCSTPGPD IKLYPFIYHA
961 VESCTQTTNQ PGQRTGA
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(2) INFORMATION FOR SEQ ID NO: 3:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4069 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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121 gctctccgcg gggccggccc ggggacagtg cgctgctggt cccagcatga atgcgggccc
181 cggctgtgaa ccctgcacca aagcgacccg ctggggcgcc gctacaactt cgccggctgc
241 ttcggacgcc cggagctttc cgagcaggca gaggcgcgtc ctcgacccca aggacgctca
301 cgtgcagttc agggtcccac cgtcctcgcc agcctgcgtc ccagggcagg cgggacagca
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 421 taaaggaatc aagacagcgg aatcagaaag tttggatagt aaagaaaaca acaatacaag
 481 aatagaatcc atgatgagtt ctgtacaaaa agataacttt taccaacata atgtagaaaa
 541 attagtaaat gtttctcagc taagtcttga taagtcactc actgaaaaaa gtacacagta
 601 tttgaaccag catcagactg cagcaatgtg taagtggcaa aatgaaggga aacacacgga
 661 gcagcttttg gaaagtgaac ctcaaacagt aaccctggta ccagagcagt ttagtaatgc
 721 taacattgat cggtcacctc aaaatgatga tcacagtgac acagatagtg aagagaatag
 781 agacaatcaa cagtttctca caactgtaaa gcttgcaaat gcaaagcaga ctacggaaga
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 961 tgttggctct gaggatgttg gtactgggtc aaaaaatgac aacaaattga ttagacaaga
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3661 tttatttaag atagaataat ttccagaaat tgtacttttg aggtatcatt tttatctgta
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3781 ctgagatgaa aggaaatgtg gaataaaagg aggtttttcct gatgtggtgt aaagaaaaca
3841 gattccaaga gaattgaaga ttttttttgt ttccttggta cttttttctt tttaaattag
3901 gactaatgtt tcttttgtgg tgcttgaggc atattcatat aaccaaagtt tgagaactgg
3961 gaacttcatg ctgatttgta catattgaag tttctctggt attcaaaggt tatatagtga
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(2) INFORMATION FOR SEQ ID NO: 4:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 976 amino acids
        (B) TYPE: protein
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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121  HNVEKLVNVS QLSLDKSLTE KSTQYLNQHQ TAAMCKWQNE GKHTEQLLES EPQTVTLVPE
181  QFSNANIDRS PQNDDHSDTD SEENRDNQQF LTTVKLANAK QTTEDEHARE AKSHQKCSKS
241  CHPGEDCASC QQDEIDVVPK SPLSDVGSED VGTGSKNDNK LIRQESCLGN SPPFEKESEP
301  ESPMDVDNSK NSCQDSEADE ETSPGFDEQE DGSSSQTANK PSRFQARDAD IEFRKRYSTK
361  GGEVRLHFQF EGGESRTGMN DLNAKLPGNI SSLNVECRNS KQHGKKDSKI TDHLMRLPKA
421  EDRRKEQWET KHQRTERKIP KYVPPHLSPD KKWLGTPIEE MRRMPRCGIR LPLLRPSANH
481  TVTIRVDLLR AGEVPKPFPT HYKDLWDNKH VKMPCSEQNL YPVEDENGER TAGSRWELIQ
541  TALLNKFTRP QNLKDAILKY NVAYSKKWDF TALIDFWDKV LEEAEAQHLY QSILPDMVKI
601  ALCLPNICTQ PIPLLKQKMN HSITMSQEQI ASLLANAFFC TFPRRNAKMK SEYSSYPDIN
661  FNRLFEGRSS RKPEKLKTLF CYFRRVTEKK PTGLVTFTRQ SLEDFPEWER CEKPLTRLHV
721  TYEGTIEENG QGMLQVDFAN RFVGGGVTSA GLVQEEIRFL INPELIISRL FTEVLDHNEC
781  LIITGTEQYS EYTGYAETYR WSRSHEDGSE RDDCERRCTE IVAIDALHFR RYLDQFVPEK
841  MRRELNKAYC GFLRPGVSSE NLSAVATGNW GCGAFGGDAR LKALIQILAA AAAERDVVYF
901  TFGDSELMRD IYSMHIFLTE RKLTVGDVYK LLLRYYNEEC RNCSTPGPDI KLYPFIYHAV
961  ESCAETADHS GQRTGT
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(2) INFORMATION FOR SEQ ID NO: 5:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3814 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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 361 aaagataact tttacccaca taaggtggaa aaattggaaa atgttcctca gctaaatctt
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 601 gaccacagtg acacagatca tgaagaagac agagacaatc agcagtttct tacacctata
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 841 gacaacaaat tgactggaca agaaagcagc ctaggtgatt cgcctccatt tgagaaagaa
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1021 aataaacttt caagttgcca agcaagagaa gctgatggcg atcttaggaa acggtatttg
1081 actaagggaa gtgaagttag attgcatttc caatttgaag gagaaaataa tgctgggacc
1141 agtgacttaa atgccaagcc atctggaaac tcttctagcc ttaatgtaga gtgtagaagt
1201 tccaagcagc atggaaaaag ggattctaaa attacagatc atttcatgag aatttccaag
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1321 ccaaaataca tcccacctaa cctccctcca gagaagaagt ggctgggaac tcctattgag
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1561 ttgtaccctg tggaagatga gaatggtgag cgaactgcag ggagtaggtg ggagctcatt
1621 cagactgcac ttctcaacaa attcacacga ccccagaact tgaaggatgc gattctgaaa
1681 tacaatgtgg catattctaa gaaatgggac tttacagctt tggttgattt ctgggataag
1741 gtacttgaag aagcagaggc ccaacattta tatcagtcca ttttacctga catggtgaaa
1801 attgcactct gtctgccaaa tatttgcacc cagccaatac cactcctgaa acagaagatg
1861 aatcattctg tcacgatgtc acaggaacag atcgccagtc ttttagctaa tgctttcttc
1921 tgcacatttc cccgacggaa tgccaagatg aaatcggagt attctagtta cccagacatt
1981 aacttcaatc ggttgtttga aggacgttca tcaaggaaac cagaaaaact gaaaacactc
2041 ttctgctact ttcgaagagt cacagagaaa aaacctacag gattggtgac atttacaaga
2101 cagagtcttg aagattttcc agaatgggaa aggtgtgaaa agcctctgac acgcttacac
2161 gtcacttacg agggtaccat agaaggcaac ggccgaggca tgctacaggt ggattttgca
2221 aatcgttttg ttggaggtgg tgtgactggt gcgggacttg tacaagaaga aatcagattt
2281 ttaatcaatc ctgaattgat tgtttcacgg ctgttcactg aggtgctgga tcacaatgag
2341 tgtcttatta tcacaggtac tgaacagtac agtgaataca caggctatgc tgaaacttat
2401 cgttgggccc gaagccatga agatgggagt gaaaaggacg attggcagcg gcgctgcacg
2461 gagatcgttg ccattgacgc acttcacttc agacgctacc tcgatcagtt tgtgcctgag
2521 aaagtgagac gtgagcttaa caaggcttac tgcggattcc tccgtcctgg agttccttct
2581 gaaaatcttt ctgcagtggc cacgggaaac tggggctgtg gtgcctttgg gggtgacgct
2641 agattaaaag ccttaataca gatcctggca gctgctgcgg ctgaacgtga cgtggtttat
2701 ttcacctttg gggactcaga gttgatgaga gacatttaca gcatgcacac tttccttacc
2761 gagaggaagc tggatgttgg aaaagtgtac aagttattgc ttagatacta caatgaagaa
2821 tgcagaaact gttccacccc tggaccagac atcaagcttt atccattcat ataccatgct
2881 gttgagtcaa gtgcagagac cactgacatg ccaggacaga aggcaggcac ctgaggaaca
2941 agtgactagg acctcctctc aaagagacat cctatttgaa atgtggggtg tgatgtctga
3001 attgactgaa tctgatctaa gtgtgtatat aatccacatt tgtaatcaag gatgcagtct
3061 cttctgcata tgcagttgtt tcttgttcat cctggtggac atgcctttag acatggcttc
3121 ttcaattttt cttctccttc agtctttatt ctttgatttt tttttccaa cttgatttct
3181 tgggaaaact caagaaaggt tgcactcagc ttctagatct ttctcttcct gtctgtgtgt
3241 tgtccagact gctttggtgg ctagcagata ccatcacact tggaggaagt tacaaatcca
3301 gaaatctgag tttgctgcag atttacctgt gagcttctca ctcccaaccc ttgttaggct
3361 tgtgttgtct acattttcaa ttttggaagt tgaagttttt cttatgttac ttaatgctag
3421 tatctttttag gctaaaacta ttttctattt aaggcagact aatttccagt ttctcttttg
3481 aaacatcatc cctataagta acggtttttt tcgtcctttt ttccccagcg ctattttaga
3541 agctggccaa gaggaaagaa aatgtagaat aaaaggattt tcctcggatg ctataaagaa
3601 gccaggttca agagcgttgg ggtttttgtt tttttcaaga cttgtttttc ctttgcagct
3661 agggtgagtg cttgttctgt ggtgctgagg gcatagtcct gtaaccaaag gtctttgctg
3721 gagacttgat gctgatttgt acatatggaa gtttctctgg caggaaatat tagagttaat
3781 aaatttcatt aataaatcat ttgtcagaaa aaaa
```

(2) INFORMATION FOR SEQ ID NO: 6:
        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 968 amino acids
             (B) TYPE: protein
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
1    MSAGPGWEPC TKARWGAAGT SAPTASDSRS FPGRQRRVLD PKDAPVQFRV PPSSPACVSG
61   RAGPHRGNAT SFVFKQKTIT TWMDTKGPKT AESESKENNN TRIDSMMSSV QKDNFYPHKV
121  EKLENVPQLN LDKSPTEKSS QYLNQQQTAS VCKWQNEGKH AEQLLASEPP AGTPLPKQLS
181  NANIGQSPHT DDHSDTDHEE DRDNQQFLTP IKLANTKPTV GDGQARSNCK CSGSRQSVKD
241  CTGCQQEEVD VLPESPLSDV GAEDIGTGPK NDNKLTGQES SLGDSPPFEK ESEPESPMDV
301  DNSRNSCQDS EADEETSPVF DEQDDRSSQT ANKLSSCQAR EADGDLRKRY LTKGSEVRLH
361  FQFEGENNAG TSDLNAKPSG NSSSLNVECR SSKQHGKRDS KITDHFMRIS KSEDRRKEQC
421  EVRHQRTERK IPKYIPPNLP PEKKWLGTPI EEMRKMPRCG IHLPSLRPSA SHTVTVRVDL
481  LRAGEVPKPF PTHYKDLWDN KHVKMPCSEQ NLYPVEDENG ERTAGSRWEL IQTALLNKFT
```

569823.5   75

```
541 RPQNLKDAIL KYNVAYSKKW DFTALVDFWD KVLEEAEAQH LYQSILPDMV KIALCLPNIC
601 TQPIPLLKQK MNHSVTMSQE QIASLLANAF FCTFPRRNAK MKSEYSSYPD INFNRLFEGR
661 SSRKPEKLKT LFCYFRRVTE KKPTGLVTFT RQSLEDFPEW ERCEKPLTRL HVTYEGTIEG
721 NGRGMLQVDF ANRFVGGGVT GAGLVQEEIR FLINPELIVS RLFTEVLDHN ECLIITGTEQ
781 YSEYTGYAET YRWARSHEDG SEKDDWQRRC TEIVAIDALH FRRYLDQFVP EKVRRELNKA
841 YCGFLRPGVP SENLSAVATG NWGCGAFGGD ARLKALIQIL AAAAAERDVV YFTFGDSELM
901 RDIYSMHTFL TERKLDVGKV YKLLLRYYNE ECRNCSTPGP DIKLYPFIYH AVESSAETTD
961 MPGQKAGT
```

(2) INFORMATION FOR SEQ ID NO: 7:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2781 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
   1 tcgaagtgtg tggtatttat aaagtgcgat attcatcaca gctatcgctc atccccaaaa
  61 caccggtatg caagaattca ggtcacactt gattttccg atattccaaa aggtttacca
 121 atctacggca aatcgccgca gagcaagtgc atccgtgctg accaatcgac tcggcaaggc
 181 tttgtgctta aactgcgcca ggatgtcgaa gtcgccggat ggcgggattt ccgaaataga
 241 aacggaggag gagccggaaa atctggcgaa ctccctagat gattcgtggc gtggagtttc
 301 catggaggct atacatcgta atcggcagcc tttcgaattg gagaatttgc caccagtgac
 361 tgccggcaat ctccaccggg ttatgtacca gctgccaatt cgtgaaacac cgccacgccc
 421 ctacaaatca ccgggaaagt gggactccga gcatgtgcgt ctgccctgtg cgcccgagtc
 481 gaaatatccg agggagaatc cggatggcag caccaccatc gattttcgct gggaaatgat
 541 cgaacgagcc cttctgcagc ccataaagac gtgtgaggaa ctgcaggcgg cgataatatc
 601 atataatacc acctatgggg atcagtggca ctttcgtgcc cttcatcaac ttctcgacga
 661 ggaactggac gagagcgaaa cacgggtttt cttcgaggat ctattgccgc gcattatccg
 721 attggcattg cggctaccgg acttgattca atcgccagtt ccgctgctca agcaccacaa
 781 gaacgcctca ttgagcctga gccaacagca gatctcctgc ctgttggcca atgccttctt
 841 gtgcacgttt ccccgaagaa acaccctcaa gaggaagtcc gagtacagca ctttttccaga
 901 catcaacttt aacaggcttt accaatcgac gggaccggca gttctggaga agcttaaatg
 961 cattatgcac tattttcgtc gcgtgtgtcc cacagagcgg gatgccagca atgtgcccac
1021 cggtgtggta accttttgttc gtcggagcgg attgccggaa catctgatcg actggagcca
1081 aagtgcggcg ccgttgggtg atgtgccatt gcacgtggat gccgagggaa caatcgagga
1141 tgagggcatt ggactgctgc aagtagactt tgccaacaaa tatttgggtg gcggtgtctt
1201 gggacatggc tgcgttcagg aggagatacg ctttgttatc tgtccggagc tattggtggg
1261 taaactcttt acggagtgtc tgcgaccatt cgaggccctg gtgatgttgg gcgccgaaag
1321 gtatagtaac tatacgggat atgccggaag cttcgagtgg tccggcaact ttgaggattc
1381 aacgccaaga gatagctcag gtcgtcgaca aacggccatt gtggcaatcg atgccctaca
1441 ttttgcccag tcacatcatc aatatcgcga ggatctcatg gaaagggagc tgaacaaggc
1501 gtacattgga tttgttcact ggatggtgac gccgccaccg ggtgtggcaa ctggtaactg
1561 gggttgcggc gcattcggcg gtgactccta tctgaaagcc ctgctgcaac ttatggtctg
1621 cgcccagttg ggcagacctt tggcctacta tacctttgga aatgtggagt ttagggatga
1681 ttttcatgaa atgtggctgt gtttcgaaa tgacgggact acggtgcagc agctttggag
1741 tattttaagg tcgtacagta ggcttattaa ggagaagagc tccaaggagc cgcgtgagaa
1801 taaggcatcc aaaaagaagc tatatgattt tattaaagag gaacttaaga aggtcagaga
1861 tgtgcccgga gagggagcat ccgccgaagc tggaagctct agagtagctg gattaggcga
1921 aggaaaatca gaaacatcag cgaaatcctc gccagaactc aacaagcaac ccgcccgacc
1981 gcaaatcacc ataacgcaac aaagtaccga tctattgccc gcgcaattat cgcaagataa
2041 ctctaattct tcggaagatc aggcccttct tatgctgtcg gacgatgagg aggccaatgc
2101 catgatggag gccgctagtc tggaggctaa aagcagcgta gaaataagca acagcagcac
2161 aacgtccaaa acgagcagta cagccacgaa atcaatgggt tcaggtggcc gccagttgag
2221 tctgctcgag atgctggaca cccattatga aaagggttcg gcctcgaaga ggccacgaaa
2281 atcacccaac tgcagcaagg ctgagggttc agcaaagagt cgtaaggaga tcgatgtgac
2341 cgacaaggac gaaaaggacg atattgttga ctaggtgata ttgcactaca ggattgttac
2401 tgcccccaaa aattgaagag gtataaaatg tattgtagat aactttaagg acatatttag
2461 ggcatttttaa agtaggatca ttgtaagtcg aataaagtga aattttttt tttttttaat
```

76

2521 tatactattc taatctgcaa agacaatttt actgttaaat ttgtataaca ttcgaattaa
2581 ttaatataat ttgttatatc atgcaaatct agcttttatt atgcgaaatt tgtagttaaa
2641 gccagtaaag tttctttta tttaaccgaa accttttgtt tatttatt gaccacaaca
2701 agaacatcaa caacaacaac cacgaaaaaa aagcgaatat atatttgttt gttcgtatat
2761 atatatatat ctaagcagat c

(2) INFORMATION FOR SEQ ID NO: 8:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 768 amino acids
        (B) TYPE: protein
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
1    MQEFRSHLIF PIFQKVYQST ANRRRASASV LTNRLGKALC LNCARMSKSP DGGISEIETE
61   EEPENLANSL DDSWRGVSME AIHRNRQPFE LENLPPVTAG NLHRVMYQLP IRETPPRPYK
121  SPGKWDSEHV RLPCAPESKY PRENPDGSTT IDFRWEMIER ALLQPIKTCE ELQAAIISYN
181  TTYRDQWHFR ALHQLLDEEL DESETRVFFE DLLPRIIRLA LRLPDLIQSP VPLLKHHKNA
241  SLSLSQQQIS CLLANAFLCT FPRRNTLKRK SEYSTFPDIN FNRLYQSTGP AVLEKLKCIM
301  HYFRRVCPTE RDASNVPTGV VTFVRRSGLP EHLIDWSQSA APLGDVPLHV DAEGTIEDEG
361  IGLLQVDFAN KYLGGGVLGH GCVQEEIRFV ICPELLVGKL FTECLRPFEA LVMLGAERYS
421  NYTGYAGSFE WSGNFEDSTP RDSSGRRQTA IVAIDALHFA QSHHQYREDL MERELNKAYI
481  GFVHWMVTPP PGVATGNWGC GAFGGDSYLK ALLQLMVCAQ LGRPLAYYTF GNVEFRDDFH
541  EMWLLFRNDG TTVQQLWSIL RSYSRLIKEK SSKEPRENKA SKKKLYDFIK EELKKVRDVP
601  GEGASAEAGS SRVAGLGEGK SETSAKSSPE LNKQPARPQI TITQQSTDLL PAQLSQDNSN
661  SSEDQALLML SDDEEANAMM EAASLEAKSS VEISNSSTTS KTSSTATKSM GSGGRQLSLL
721  EMLDTHYEKG SASKRPRKSP NCSKAEGSAK SRKEIDVTDK DEKDDIVD
```


(2) INFORMATION FOR SEQ ID NO: 9:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2181 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
1    ATGAGCAAGA AGTTTATCGA ACTGGGTGAT CCTGTCACTC AAGACGAGAA
51   AGACTACGAA GACTATGTCG GAGTTGGTTT CGCGCATCAA GTCCCGACAA
101  TGAAAAGGCG GAAGTTGACA GAACATGGAA ATACTACAGA ATCAAAAGAA
151  GATCCTGAAG AGCCAAAAAG CCGTGACGTA TTTGTCTCCT CGCAGTCAAG
201  TGATGAGAGT CAAGAAGATT CGGCTGAAAA TCCGGAGATC GCTAAAGAAG
251  TGTCAGAAAA TTGTGAAAAT CTGACAGAAA CTCTCAAAAT TTCTAATATT
301  GAGAGTTTGG ACAATGTTAC TGAAAGATCT GAACACACTC TTGATAATCA
351  CAAAAGTACT GAACCAATGG AAGAAGATGT AAACAACAAG TCCAATATTG
401  ACGTTGCGAT TAATTCTGAC GAGGATGATG AACTTGTTCT GGAAGAGAAT
451  AATAAAGAAA TGAGGGATGG AGAACAAGTA CAACAGTTGT CACAGGATTT
501  ATTCGCTGAT GATCAAGAGC TAATTGAATA TCCAGGAATT ATGAAAGACA
551  CTACAACTCA ACTGGATATA ACAGATTCTG AAGTGGAGAC TGCTCAAAAA
601  ATGGAAATGA TTGAAGAAAC TGAAGCAGAT TCGACATTTG TAGGCGAGGA
651  TTCAAAAGCT ACGAAAACTG TGAGGACATC CAGTTCAAGT TTCCTGTCAA
701  CTGTTTCAAC ATGCGAAGCC CCTGCAAAAG GACGAGCAAG AATGTATCAA
751  AAAGAGTTGG AAAAGCATGT GATTGCATTT ACTGAGGGAA ATCTCACACT
801  ACAACCAGAT TTGAACAAAG TTGATCCCGA CAGAAACTAT CGATATTGTA
851  CAATTCCGAA CTTTCCAGCT TCCCAAGGAA AACTTCGAGA AGATAATCGA
901  TATGGCCCAA AAATCGTTTT GCCTCAAAGA TGGCGAGAAT TTGATTCGAG
951  GGGCCGTAGA AGAGACTCAT ATTTCTATTT CAAACGTAAG CTCGATGGAT
```

```
1001  ATTTGAAATG CTACAAAACA ACTGGATATT TTATGTTTGT TGGACTTTTG
1051  CACAACATGT GGGAATTTGA CCCAGACATC ACATATAAAC TGCCAGCACT
1101  GGAAATGTAT TACAAAGAGA TGTCGGAACT TGTTGGTAGA GAAGAGGTTT
1151  TGGAAAAATT TGCACGAGTT GCCCGCATCG CAAAAACTGC TGAAGATATT
1201  CTGCCAGAGC GAATTTATCG TCTTGTTGGT GACGTCGAAT CAGCTACCTT
1251  GAGCCACAAG CAATGTGCTG CACTTGTTGC GAGAATGTTT TTTGCCCGAC
1301  CGGACAGTCC TTTCAGTTTC TGCCGAATTC TCTCGTCTGA TAAATCTATT
1351  TGTGTGGAGA AACTTAAATT CCTGTTCACT TATTTCGACA AAATGTCAAT
1401  GGATCCACCG GATGGTGCCG TCAGTTTTAG ACTTACAAAA ATGGATAAAG
1451  ATACGTTCAA CGAAGAGTGG AAAGATAAAA AATTACGTTC TCTTCCTGAA
1501  GTTGAATTCT TTGATGAAAT GCTTATTGAA GACACAGCTC TCTGTACACA
1551  AGTTGATTTT GCGAACGAAC ATCTTGGTGG CGGAGTTTTA AATCATGGGT
1601  CTGTTCAGGA GGAGATCCGT TTCTTGATGT GTCCAGAAAT GATGGTTGGA
1651  ATGTTGTTGT GCGAGAAAAT GAAACAACTG GAAGCGATTT CAATTGTTGG
1701  AGCTTACGTT TTCAGTTCTT ATACTGGTTA TGGTCATACT CTAAAATGGG
1751  CAGAACTTCA ACCAAATCAT TCTCGTCAGA ATACAAACGA ATTTCGAGAT
1801  CGTTTTGGAC GTCTTCGGGT AGAAACTATT GCAATCGATG CAATTCTGTT
1851  CAAAGGATCA AAATTAGATT GTCAGACGGA GCAGTTAAAC AAAGCAAATA
1901  TCATTAGGGA AATGAAGAAA GCATCTATCG GATTCATGAG CCAGGGACCG
1951  AAATTCACAA ATATTCCAAT TGTTACTGGA TGGTGGGGAT GTGGAGCATT
2001  TAATGGGGAC AAGCCACTGA AGTTCATAAT CCAAGTAATT GCTGCCGGAG
2051  TCGCTGATCG TCCACTTCAT TTCTGTTCAT TTGGAGAACC CGAGCTTGCC
2101  GCAAAGTGCA AGAAAATTAT AGAACGAATG AAACAGAAGG ACGTAACACT
2151  TGGTAAGTCA TGTTTTTCAA TCTTCAGTTG A
```

(2) INFORMATION FOR SEQ ID NO: 10:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 726 amino acids
         (B) TYPE: protein
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
  1  MSKKFIELGD PVTQDEKDYE DYVGVGFAHQ VPTMKRRKLT EHGNTTESKE DPEEPKSRDV
 61  FVSSQSSDES QEDSAENPEI AKEVSENCEN LTETLKISNI ESLDNVTERS EHTLDNHKST
121  EPMEEDVNNK SNIDVAINSD EDDELVLEEN NKEMRDGEQV QQLSQDLFAD DQELIEYPGI
181  MKDTTTQLDI TDSEVETAQK MEMIEETEAD STFVGEDSKA TKTVRTSSSS FLSTVSTCEA
241  PAKGRARMYQ KELEKHVIAF TEGNLTLQPD LNKVDPDRNY RYCTIPNFPA SQGKLREDNR
301  YGPKIVLPQR WREFDSRGRR RDSYFYFKRK LDGYLKCYKT TGYFMFVGLL HNMWEFDPDI
361  TYKLPALEMY YKEMSELVGR EEVLEKFARV ARIAKTAEDI LPERIYRLVG DVESATLSHK
421  QCAALVARMF FARPDSPFSF CRILSSDKSI CVEKLKFLFT YFDKMSMDPP DGAVSFRLTK
481  MDKDTFNEEW KDKKLRSLPE VEFFDEMLIE DTALCTQVDF ANEHLGGGVL NHGSVQEEIR
541  FLMCPEMMVG MLLCEKMKQL EAISIVGAYV FSSYTGYGHT LKWAELQPNH SRQNTNEFRD
601  RFGRLRVETI AIDAILFKGS KLDCQTEQLN KANIIREMKK ASIGFMSQGP KFTNIPIVTG
661  WWGCGAFNGD KPLKFIIQVI AAGVADRPLH FCSFGEPELA AKCKKIIERM KQKDVTLGKS
721  CFSIFS
```

(2) INFORMATION FOR SEQ ID NO: 11:
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 31 amino acids
         (B) TYPE: polypeptide
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein fragment

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

LFTEVLDHNE CLIITGTEQY SEYTGYAETY R

(2) INFORMATION FOR SEQ ID NO: 12:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 amino acids
        (B) TYPE: polypeptide
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein fragment

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AYCGFLRPGV SSENLSAVAT GNXGCGAFG

(2) INFORMATION FOR SEQ ID NO: 13:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11 amino acids
        (B) TYPE: polypeptide
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein fragment

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

FLINPELIVS R

(2) INFORMATION FOR SEQ ID NO: 14:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 amino acids
        (B) TYPE: polypeptide
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein fragment

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

IALXLPNIXT QPIPLL

(2) INFORMATION FOR SEQ ID NO: 15:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 amino acids
        (B) TYPE: polypeptide
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein fragment

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GAYCAYAAYG ARTGYYT

(2) INFORMATION FOR SEQ ID NO: 16:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 amino acids
        (B) TYPE: polypeptide
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein fragment
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
CKRTANGTYT CNGCRTA

(2) INFORMATION FOR SEQ ID NO: 17:
         (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 24 bases
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: oligonucleotide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATCATCACAG GTACTGAGCA GTAC

(2) INFORMATION FOR SEQ ID NO: 18:
         (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 24 bases
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: oligonucleotide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTGTGTAT TCACTGTACT GCTC

(2) INFORMATION FOR SEQ ID NO: 19:
         (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 amino acids
                (B) TYPE: polypeptide
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: polypeptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

EDKRKEQCEM KHQRTERKIP KYIPPH

(2) INFORMATION FOR SEQ ID NO: 20:
         (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 amino acids
                (B) TYPE: polypeptide
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: polypeptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

EDRRKEQWET KHQRTERKIP KYVPPH

(2) INFORMATION FOR SEQ ID NO: 21:
         (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 amino acids
                (B) TYPE: polypeptide
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: polypeptide
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

EDRRKEQCEV RHQRTERKIP KYIPPN

(2) INFORMATION FOR SEQ ID NO: 22:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 32 amino acids
                (B) TYPE: polypeptide
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: polypeptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

HQVPTMKRRK LTEHGNTTES LLLKEDPPEP KS

(2) INFORMATION FOR SEQ ID NO: 23:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 amino acids
                (B) TYPE: polypeptide
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: polypeptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

EGKRKGDEVD GVDEVAKKKS KKEKDK

(2) INFORMATION FOR SEQ ID NO: 24:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 amino acids
                (B) TYPE: polypeptide
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: polypeptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

EGKRKGDEVD GTDEVAKKKS RKETDK

(2) INFORMATION FOR SEQ ID NO: 25:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 amino acids
                (B) TYPE: polypeptide
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: polypeptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

EGKRKGDEVD GIDEVTKKKS KKEKDK

(2) INFORMATION FOR SEQ ID NO: 26:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 25 amino acids
                (B) TYPE: polypeptide
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: polypeptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

EGKRKGEEVD GNVVAKKKSR KEKEK

(2) INFORMATION FOR SEQ ID NO: 27:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 amino acids
        (B) TYPE: polypeptide
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: polypeptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

EGKRKADEVD GHSAATKKKI KKEKEK

(2) INFORMATION FOR SEQ ID NO: 28:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 amino acids
        (B) TYPE: polypeptide
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: polypeptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

EELPDTKRAK MELSDTNEEG EKKQR

(2) INFORMATION FOR SEQ ID NO: 29:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 amino acids
        (B) TYPE: polypeptide
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: polypeptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

EGVSSAKKAK IEKIDEEDAA SIKELTEKIK K

(2) INFORMATION FOR SEQ ID NO: 30:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 28 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: oligonucleotide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCTGCGGGTC TCGACGATGA GTGCGGGC

(2) INFORMATION FOR SEQ ID NO: 31:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: oligonucleotide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GCGTCTAGAA TTCACTTGGC TCCTCAGGC

(2) INFORMATION FOR SEQ ID NO: 32:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 38 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: oligonucleotide

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CCGGAATTCG GGTTTTTTGT TAATGAAAAT TTATTAAC

(2) INFORMATION FOR SEQ ID NO: 33:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 29 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: oligonucleotide

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TCAGAGCAGA TGAACTCGAG CAGTCCAGG

(2) INFORMATION FOR SEQ ID NO: 34:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 61 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: oligonucleotide

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

1 CCAATTTGAA GGAGGAATTC CCGCCGCCAC CATGAATGAT GTGAATGCCA AACGACCTGG
61 A

(2) INFORMATION FOR SEQ ID NO: 35:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: oligonucleotide

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

gaattcccgc cgccaccATG AA

(2) INFORMATION FOR SEQ ID NO: 36:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 674 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
     1    agaagaaaat ggccaaggca tgctacaggt ggattttgca aatcgttttg ttggaggtgg
    61    tgtaaccagt gcaggacttg tgcaagaaga aatccgcttt ttaatcaatc ctgagttgat
   121    tatttcacgg ctcttcactg aggtgctgga tcacaatgaa tgtctaatta tcacaggtac
   181    tgagcagtac agtgaataca caggctatgc tgagacatat cgttggtccc ggagccacga
   241    agatgggagt gaaagggacg actgcgagcg gcgctgcact gagatcgttg ccatcgatgc
   301    tcttcacttc agacgctacc tcgatcagtt tgtgcctgag aaaatgagac gcgagctgaa
   361    caaggcttac tgtggatttc tccgtcctgg agtttcttca gagaatcttt ctgcagtggc
   421    cacaggaaac tggggctgtg gtgcctttgg gggtgatgcc aggttaaaag ccttaataca
   481    gatattggca gctgctgcag ctgagcgaga tgtggtttat ttcacctttg gggactcaga
   541    attgatgaga gacatttaca gcatgcacat tttccttact gaaaggaaac tcactgttgg
   601    agatgtgtat aagctgttgc tacgatacta caatgaagaa tgcagaaact gttccacccc
   661    tggaccagac atca
```

(2)   INFORMATION FOR SEQ ID NO: 37:
      (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 200 bases
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
     1    aaaaatagtt gtcaagactc agaagcagat gaggagacaa gtccaggttt tgatgaacaa
    61    gaagatggta gttcctccca aacagcaaat aaaccttcaa ggttccaagc aagagacgct
   121    gacattgaat ttaggaaacg gtactctact aagggcggtg aagttagatt acatttccaa
   181    tttgaaggag gagagagtcg
```

(2)   INFORMATION FOR SEQ ID NO: 38:
      (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 29793 base pairs
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
     1    gatctcgaag taaaaactca cgcagaaaga gctcctcctc ctttagcatg agaatccaac
    61    tttgtaatga taacactggc aacatcaaca gtttgagaga aagcacgtgc ttgggcttca
   121    caagcttgtc caatagaagc atccatcaca aaaacaacat tatctggtgt aactgcgttg
   181    gaaacttgga gcatttcttc gaaaagtgaa gcttcttgct tgtgacgacc tgatgtatca
   241    acaatgatga tttcgaaccc ttcttgctgc aaaacaaata ttattaaacc atttttctgt
   301    gataaattac cgtgaatttt tctactcctt cggcggcaat ttttacgggg tcaatttcag
   361    agtatgatcc atagaaggga atacgagctt ttgtggcatt ttgctttaat·tgatcaaaag
   421    ctccagcacg gaatgtatcg gcacagatca gacatgtttt ccatcctttt ctttggtagt
   481    aatacgccat ctgaacttga aaagtgttga aaagttgttg gaagtttact aattaaaaaa
   541    tataatgttt gatggtgtgt gagctttcta ttgtaattca tggaacgaac cttggtacaa
   601    gtcgtagttt taccggaacc ttgaagacca acaaacatga aaacgttgcg acgtcctttt
   661    gttggtgtga aaggagttac accaggatcc acaagcttca gcagttcatt gaatactgtc
   721    ttctgaatgt accgacgttt gtttgctcct ccgacgatct cttcgaaatt aatcgctttt
   781    ctgaaaatat ttattaaatt taaatcttaa atagcgtaaa aatttacttc acgttgtcct
   841    taagttgctt tacaagacga atatgaacat cagattcaat aagagctgta cagacttctt
   901    tcagcatcaa atccagctcc ccctcattga taacggtgct ctgaccgagc tttccgatcg
   961    catttcggat tttccgcccc aaatcggcca aaaccatttt gaactgaaat ttgaaatgct
  1021    ttaatttgtt taagcataga attaaacgcg ttttaaatcg agagcaccat aaaaacagtt
  1081    tggagaaaaa tcgataattc ttgtaggaga ttcagtccct gtggtttttct tcggcttcct
  1141    aatcattttt tgacgacata gtggtatttc acataggtt ttttcaagac acaacagatt
  1201    tttcacaaag agtagagaag aaatggaaaa ctgtagattt cttctcgaag agccgagaaa
  1261    ggcaaggtat tggaagttta aaaaggtaat gtttctttat tcttttttca aaacaataat
```

```
1321  aaatggaaaa  tatatattta  tagataacaa  tttcagacag  ttaaaatcac  gtgaaaaatt
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1441  ttgcgcgttt  gacgatttta  ttgacgcgtt  tctggtgcat  gcgggaaatt  ttttattttc
1501  aacttttttc  ctgtttgttt  atcctttttt  aattgaattc  tcatgatttg  aaagctttga
1561  aaaatattat  tttgctcaaa  aacatgcgtt  ttgtaaaaca  ttgattagat  tcaaggcaat
1621  taatggattt  ttgcacgttc  caaaaaaaag  gaaattcatt  ttttgaaaat  tttgataatt
1681  taataatgaa  aaatgttcca  tagatttatt  caatgccatc  cttctctata  atctcgaact
1741  tccgcatcct  tcaactgtgg  tagaggtatt  tgcaatacca  tatagtcgta  ataataaact
1801  ttagtgaaca  aatccaagac  atcagctctt  gagtaaatga  atgatttata  aaaactgctg
1861  attttctcgt  aggaagaaag  agaatcagct  aataatccgt  cgttgtctat  tctgtcaggc
1921  cgcttaaatg  ttaaaaaata  aaaacgtttt  aagctaattt  tgtatgtcta  gaaactctaa
1981  ctcacaagca  tttctgcata  cgccggatta  gttggttttg  caaaaagcga  gtaatctaca
2041  aaagtgaatt  tttgattcat  ctcttccatt  tcacaaaacc  aattttgtgg  tacgtatttc
2101  atatgatctt  catccacttt  tttagttttt  gaatgtattt  gtgtgagttg  tgtccagatt
2161  tgaataagat  aacatctcag  atccaacttg  caattgaagc  aagaacgatc  ttctctgaaa
2221  ttttatatga  ccttaaactt  tatacttttg  tagtttcgtc  gatatctgat  cgttcagttg
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2521  gttaataatg  aacctcacga  ttcatcatta  aatttctctt  ggagcccgca  taatacttgc
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2641  aagatttaat  cttaagcgag  tgttctgatc  aatttaaata  tttgatactc  accgcaagtt
2701  tcttcgaaac  ttgttcgaaa  gctggaattt  tagaatatcc  ttcaaaactt  ttttcctcgc
2761  cctcatcaag  ccataataag  ttttgatcag  caatatattc  gaataaatta  gtctctgata
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2881  taattataat  tataatagtt  cgtcgctgag  ttgatgaaga  ccacataatt  agtttaatgg
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4201  aattttaggt  gtaatgttaa  ttttttgctg  tagtttttcc  cattgtttga  aattttgcc
4261  aaaattagtt  attgcatacc  cttcatgttt  ttgaagattg  tttaggaatg  agaaacatt
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4441  taaaatttct  cctaaagttt  tttgctaata  tttttcgcta  tcgcgtaatt  tactagtgaa
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4561  aaacttaaac  ttaaattttg  acaaggcgag  aggaaaaaat  taaaaattgc  tgaacattca
4621  gatgccggtt  accttatttt  tggttcaaaa  atcccaatat  tacgcgtctg  ggttatagtc
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4801  ttcttgtcac  ttcctccatt  tcgcaataat  ataactcgag  aaatatagaa  ttttgttcga
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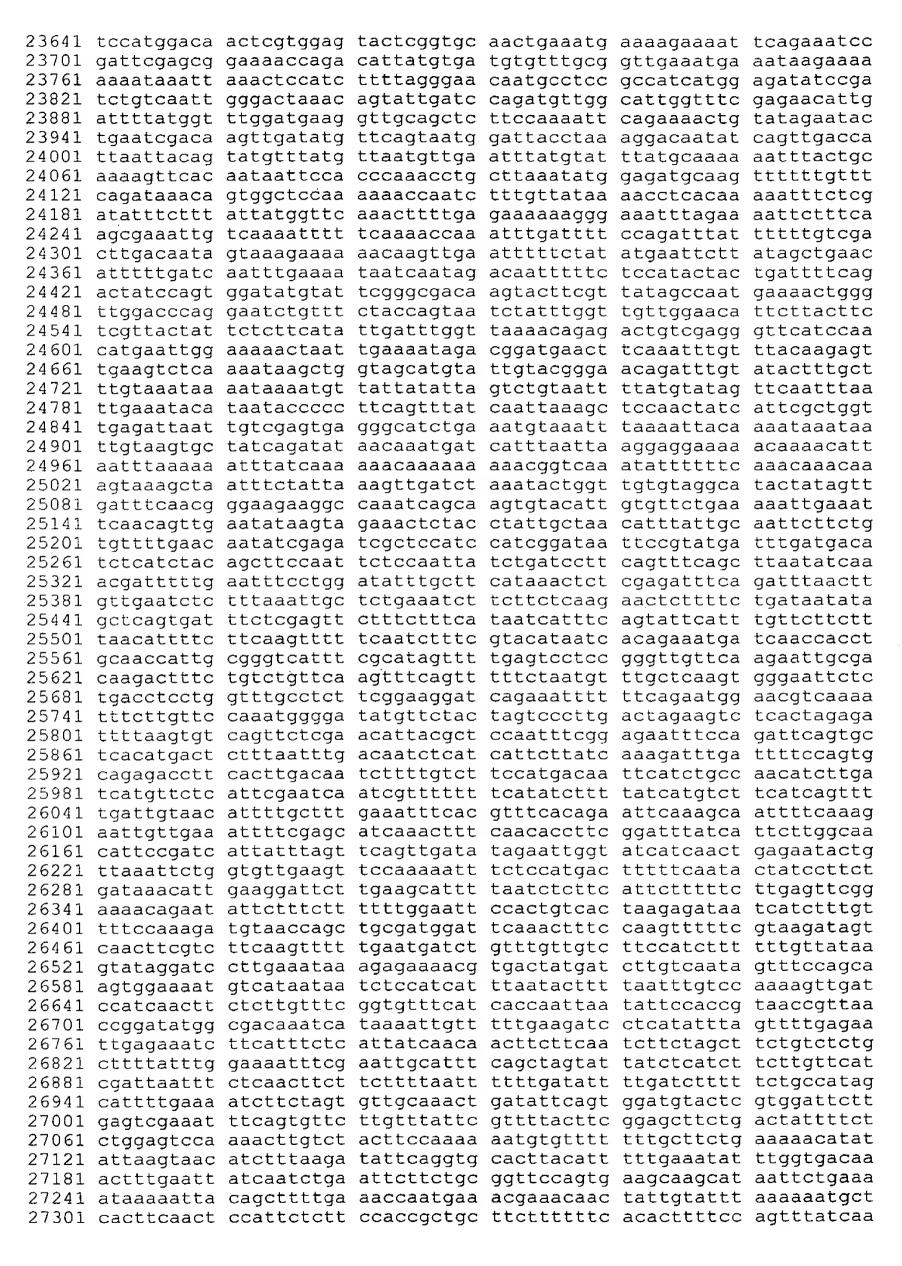
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6961  aagaataaaa caaaaggtag gcaacttgta tattcaaaat ttgacggtga ttgcaacttt
7021  taactaattt caggccattt tttgagccgt cataactttt ttctaaaaag ttttcaagaa
7081  gtttcattat gaaattcggt gttttcagac aattttgagt ctaataagga aataaaaaaa
7141  attcgagtac accacctttta agaaaatttt ggattccgc tacgctaatc caccttttaat
7201  caaaaatatt tgaagttatt caaagttaaa gaattatatt ttcagagggg ccgtagaaga
7261  gactcatatt tctatttcaa acgtaagctc gatggatatt tgaaatgcta caaaacaact
7321  ggatatttta tgtttgttgt aagttttttga aatacaattc gtttgaagat ttactctatt
7381  ttcagggact tttgcacaac atgtgggaat ttgacccaga catcacatat aaactgccag
7441  cactggaaat gtattacaaa gagatgtcgg aacttgttgg tagagaagag gttttggaaa
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7561  ttatgagata tacagcattt cctctaatag tattgcatat aaacatttca cttttgaggtt
7621  atatcttggt ttattttaaa aatatcaata aatacaaaac aatagaaaaa tgataaaaaa
7681  acattttgtc agttgataat ttgggtatag tattcattca taatttgatt tttttagcga
7741  atttatcgtc ttgttggtga cgtcgaatca gctaccttga gccacaagca atgtgctgca
7801  cttgttgcga gaatgttttt tgcccgaccg gacagtcctt tcagttctg ccggtgagta
7861  atacaagaat gctcatattt ttagaatcaa tatttgcaag gaactttaat cttacgtacg
7921  tcttaagatg agcattttcg cacatatctt acgcgcacga gtctcgacac gcgaacatcg
7981  agcttctgta actcgtatca atttacaagc cgttattaca tcagttttta atgaatttta
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8341  atgaaatgct tattgaagac acagctctct gtacacaagt tgattttgcg aacgaacatc
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8521  tggttggaat gttgttgtgc gagaaaatga acaactgga agcgatttca attgttggag
8581  cttacgtttt cagttcttat actggttatg gtaagtctag actttcaaaa aaaactgttc
8641  caatatgtca atatatttca ggtcatactc taaaatgggc agaacttcaa ccaaatcatt
8701  ctcgtcagaa tacaaacgaa tttcgagatc gttttggacg tcttcgggta gaaactattg
```

```
8761   caatcgatgc aattctgttc aaaggatcaa aattagattg tcagacggag cagttaaaca
8821   aagcaaatat cattagggaa atgaagaaag catctatcgg attcatgagc cagggaccga
8881   aattcacaaa tattccaatt gttactggat ggtgggggatg tggagcattt aatgggggaca
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